

Assessment of Genetic Divergence and Correlation Analysis of Sugarcane Clones (*Saccharum spp. L.*) in North-Western Plain Zone of Uttar Pradesh

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Abstract

Nine early maturing sugarcane clones and their 12 morpho-physiological characters were studied in 2015-16 and 2016-17 crop seasons under inorganic environment to assess their genetic distance and characters association. The results of the experiment revealed that variety CoPk 05191 had greater genetic distance from CoS03251 (239.401), CoLk011201 (227.923) and UP 05125 (201.355), medium genetic distance was between Co098014 and Co 011201 (224. 618), Co098014 and UP05125 (179.927), and Co098014 and CoS03251 (178.029). The hybridization between the aforesaid combinations of clones can produce heterotic and transgressive genotypes with higher cane and sugar yield. The cane yield showed strong positive and highly significant correlation with cane height ($r=0.948^{**}$), single cane weight ($r=0.817^{**}$), number of millable cane ($r=0.748^{**}$), and green top yield ($r=0.653^{**}$). Being highly correlated with cane yield, the characters like cane height, cane weight, NMC and green top weight need special focus while making selection for higher cane and sugar yield.

Keywords: Cluster analysis; Correlation; Dendrogram; genetic diversity; Sugarcane

Introduction

Sugarcane (*Saccharum spp. complex*) is very useful perennial herbaceous industrial crop grown across the tropical and sub-tropical regions of India. Presence of high concentration of sugar coupled with generation of bio-ethanol from sugarcane molasses enlarged the area of this cash crop in about 90 countries across the world (Prakash *et al.* 2020). Sugarcane provides variety of products such as sugar, jaggery, molasses, khandsari (brown sugar), bagasse and pressmud and also plays a crucial role in political, social and economic fabrics of Indian society. Pressmud can be utilized for bio-compost preparation to enhance the soil quality and health, while bagasse has potential role in electricity generation (Sanghera *et al.* 2015). At present sugarcane is grown in 16 million hectare area across the globe with 112 million tonnes sugar production. India is the largest producer of sugarcane among all the countries with 4.86 million hectare area under sugarcane production with 377.8 million tonnes sugarcane production (Directorate of Economics and Statistics, Govt. of India, 2019-20).

Among the Indian states, Uttar Pradesh has the largest sugarcane area and production followed by Maharashtra, Karnataka, Tamil Nadu, Andhra Pradesh, Gujarat, Bihar, Haryana and Punjab. In terms of productivity Tamil Nadu stands first with over 100 tonnes/ha among all the states followed by Karnataka, Maharashtra and Uttar Pradesh. The sucrose percentage ranges from 12 to 18% depending upon the sugarcane variety, maturity level, soil and climatic conditions and different cultural practices adopted by the growers (Singh and Singh, 2002). Sugarcane has high ability of tolerance against cold, insect-pest and disease resistance, ratoon ability and vigor; thus its clones such as Indian ($2n=64$), Glagah ($2n=112$) and Yacheng ($2n=64, 80$) have been successfully utilized for breeding programmes across the world for enhancing cane yield and improvement in other quality traits (Henry and Kole, 2010).

In addition to this, a series of elite sugarcane parents *i.e.* Co, POJ and Yacheng have been obtained from their descendants. The success of any breeding programme depends much on genetic diversity available in the crop and judicious selection of parents for resorting to hybridization aimed at creating new genetic variability, which increases the chance of obtaining transgressive genotypes in the successive segregating generations. A better understanding of the genetic diversity between the clones to be used as the progenitors of the new varieties is essential in designing and defining the new crosses (Alwala *et al.*, 2006; Santos *et al.*, 2012). Improvement of sugarcane varieties through hybridization process has encountered considerable difficulties due to narrow base of variation owing to its high polyploidy ($2n$) varying from 80-124 in cultivated genotypes and 48-150 in wild (Gulzar *et al.*, 2015).

In sugarcane, frequently aneuploidy is impeded by its complex genome, narrow gene pool, poor fertility caused by long breeding selection cycle and genetic recombination. The selection of variety is a crucial factor in sugarcane breeding and production. The yield potential, disease and pest resistance varies with different varieties and they are bred for various economic and ecological considerations (Sanghera *et al.*, 2014). Generally, the selection of parental lines in sugarcane breeding programmes have been delineated on the ground of pedigree records and agronomic characters, using polycrosses or biparental crosses between elite genotypes. In addition, repeated selection of same traits like sucrose content in breeding programmes has resulted in decreased genetic diversity in sugarcane accessions.

Mahalanobis (1936) generalized that distance has been used as an efficient tool in quantifying genetic diversity and a rational choice of potential parents for a breeding programme. Also, estimation of phenotypic and genotypic correlations among the yield parameters have macadamized the basis for selection of superior genotypes from the diverse breeding populations, thereby constituting convenient plant attributes for selection and improvement of quality traits and cane yield status of sugarcane varieties. D^2 statistics is an important tool to assess genetic divergence which occurs due to different patterns of evaluation or geographical separation or due to genetic barriers to cross ability. This technique helps in prediction of high index scores of genotypes and crossing between different clusters of maximum variability of good combinations.

As the demand of white sugar is continuously increasing owing to the burgeoning population in the country which prompts the breeders to enhance both cane productivity and sugar recovery by developing potential sugarcane clones/varieties. Varietal improvement is one of the cheapest technologies for boosting cane production, productivity and sugar recovery and this programme proceeds *via* choosing genetically diverse parents and selection of transgressive clones/ genotypes from segregating populations to evolve a new variety of choice. Present study was conducted with the objectives of establishment of genetic diversity among the selected sugarcane clones with important quality traits under sub-tropical conditions and correlation among these traits as a base for selection of superior genotypes from the diverse population.

Materials and Methods

Planting material

A total of nine clones of *Saccharum officinarum* viz. Co 0238, CoSe 03234, UP 05125, CoS 03251, Co 098014, Co 0118, CoLk 011201, CoLk 013201 and CoPk 05191 belonging to early maturing group were selected for first plants and ratoon crop during 2015-16 and 2016-17 crop seasons, respectively. These clones were collected from four different agro-ecological zones of India.

Experimental site

The field experiment was conducted during 2015-16 and 2016-17 at the research farm of ICAR-Indian Institute of Farming Systems Research, Modipuram (29°4' N Latitude and 77°46' E Longitude, Meerut, 237 m above sea level), Uttar Pradesh, India. The experimental site is a part of Upper Indo-Gangetic plain, having sandy loam texture soil (52.5% sand, 30.9% clay and 16.6% silt) of Gangetic alluvial origin, very deep (>20 m), well drained and with flat (1% slope) topography. The soil of the experimental site was *TypicUstochrept* and average monthly minimum and maximum temperatures in January (the coolest month) are 7.8°C and 20.1°C, respectively. The corresponding temperatures in May (the hottest month) are 24.2°C and 39.8°C, respectively. Average annual rainfall is 747 mm, and over 75% of this is received through the south-west monsoon during July–September.

Field experiment

The experiment was laid out in randomized block design (RBD) with the three replications keeping 60 cm row to row distance and putting 12 buds per running meter in 6.0meterlong plot. The plot size was 6×0.6m×6.0m. The experiment was conducted under inorganic conditions and nutrients were supplied through use of vermicompost, pressmud fertilizer was applied at the rate of 280 kgN/ha, 100 kgP/ha and 90 kgK/ha. Furrow irrigation was given as and when required during the growing phase. Hand weeding was done for weed control. Sampling and measurement of different quality traits were carried out in the month of November. Among the quality traits tillering 000'/ha, NMC 000'/ha, single cane weight (kg), stem girth (cm), Brix (%), Cane yield/plot (kg), Green top yield/plot (kg), cane yield tonnes/ha, Green top tonnes/ha, leaf area index and SPAD were taken at the time of harvesting.

Statistical Analysis

The dispersion of the quantitative traits were described using coefficient of variance (CV). Genetic divergence among the different values were analyzed using SPSS software. Test of significance for difference between trait means was carried out using F-table.

Results and Discussion

Variation analysis of quality traits

Identification of suitable germplasm is an important aspect of any crop improvement programme. High yielding genotypes with exceptional environmental sustainability and phenotypic characteristics can be utilized for improvement of any crop. Further, selection of genotypes with superior germplasm with advanced production quality traits is significant for higher production (Baloch *et al.* 2017). Analysis of variance for 9 genotypes revealed significant difference for all the 12 characters under the present study (Table 1). The results showed significant difference among the different genotypes for tillering, number of millable cane (NMC), single cane weight, stem girth, cane height, brix per cent, cane yield/plot, green top yield/plot, cane yield tonnes/ha, green top yield tonnes/ha, leaf area index (LAI) and SPAD reading at $P \leq 0.05$ probability level.

The obtained results exhibited that genotype CoPk05191 recorded highest number of tillers (194.30 tillering 000'/ha), NMC (156.49 000'/ha), cane and green top yield, LAI and SPAD reading among all the genotypes of sugarcane first crop. Genotypes Co0238, CoSe03234, UP05125, CoS03251 and Co0118 were found statistically at par in terms of number of tillers/ha (Table 1). Although, Co0238 was found superior among all the genotypes in terms of single cane weight (1.64 kg), stem girth (2.61 cm), cane height (250.11 cm) and brix (21.34%). This advocates that the observed genotypes possess advantageous genetic resources for variety of traits, therefore genotypes can be employed for higher production as well as breeding programmes (Khan *et al.* 2013). Similarly, genotype CoPk05191 was found superior in terms of number of tillers, NMC, cane and green top yield and SPAD reading over the other genotypes in ratoon crop. While, Brix% was found highest in case of CoSe03234 genotype followed by Co0118, UP05125 and Co098014 genotypes (Table 2).

Treatments	Tillering '000'/ha	NMC '000'/ha	Single Cane Weight Kg	Stem girth (cm)	Cane height (cm)	Brix %	Cane Yield / Plot (Kg)	Green top yield/ Plot (Kg)	Cane Yield Ton/hac	Green Top Ton/hac	Leaf Area Index	SPAD
Co 0238	89.20 ^E	78.09 ^{DE}	1.64 ^A	2.61 ^A	250.11 ^{AB}	21.34 ^{AB}	226.67 ^D	35.00 ^C	104.95 ^D	16.18 ^C	10.37 ^{AB}	43.02 ^{AB}
CoSe 03234	108.03 ^{DE}	97.56 ^{CDE}	1.35 ^B	2.24 ^{AB}	247.89 ^{AB}	21.55 ^A	248.67 ^C	51.00 ^B	115.13 ^C	23.61 ^B	9.74 ^{BC}	40.48 ^{BC}
UP 05125	106.79 ^{DE}	99.39 ^{CD}	0.78 ^E	1.64 ^C	200.33 ^{CD}	21.33 ^{AB}	170.67 ^{EF}	33.33 ^C	79.02 ^{EF}	15.43 ^C	7.38 ^E	35.55 ^C
CoS03251	82.72 ^E	73.77 ^E	1.02 ^{DE}	2.26 ^{AB}	184.22 ^D	19.94 ^{BC}	153.33 ^F	31.67 ^C	70.99 ^F	14.66 ^C	7.78 ^{DE}	42.26 ^{AB}
Co 098014	133.49 ^{BCD}	105.25 ^C	1.30 ^{BC}	2.05 ^{BC}	273.33 ^A	21.56 ^A	282.67 ^B	28.67 ^C	129.64 ^B	13.27 ^C	9.44 ^{BC}	41.39 ^B
Co 0118	115.44 ^{CDE}	97.69 ^{CDE}	1.35 ^B	2.41 ^{AB}	226.44 ^{BC}	21.31 ^{AB}	233.33 ^{CD}	51.00 ^B	108.03 ^{CD}	23.61 ^B	8.68 ^{CDE}	41.31 ^B
CoLk 011201	150.32 ^{BC}	109.73 ^{BC}	1.05 ^{CDE}	2.12 ^{BC}	227.44 ^{BC}	19.69 ^C	190.00 ^E	35.83 ^C	87.97 ^E	16.59 ^C	8.96 ^{CD}	36.09 ^C
CoLk 013201	158.19 ^{AB}	133.65 ^{AB}	1.09 ^{BCD}	2.16 ^{AB}	242.66 ^{AB}	19.53 ^C	272.67 ^B	56.20 ^{AB}	126.24 ^B	26.02 ^{AB}	11.25 ^A	43.60 ^{AB}
CoPk 05191	194.30 ^A	156.49 ^A	1.25 ^{BCD}	2.13 ^{AB}	249.77 ^{AB}	19.33 ^C	317.00 ^A	62.67 ^A	146.77 ^A	29.01 ^A	10.67 ^{AB}	46.39 ^A
Mean	126.50	105.73	1.20	2.18	233.58	20.62	232.78	42.82	107.64	19.82	9.36	41.12
CV(%)	17.22	13.30	13.09	12.75	7.93	4.16	5.19	12.08	5.04	12.09	8.41	6.99

Table 1: Means and analysis of variance for 12 yield and quality traits among 9 genotypes of sugarcane first crop.

Treatments	Tillering '000'/ha	NMC '000'/ha	Single Cane Weight Kg	Stem girth (cm)	Cane height (cm)	Brix %	Cane Yield / Plot (Kg)	Green top yield/ Plot (Kg)	Cane Yield Ton/ha	Green Top Ton/ha	Leaf Area Index	SPAD
Co 0238	102.17 ^{CD}	90.59 ^{CDE}	2.28 ^A	3.09	264.44 ^{ABC}	21.65 ^{AB}	276.67 ^{BC}	41.27 ^{CDE}	128.09 ^{AB}	19.10 ^{CDE}	10.22 ^{AB}	46.73 ^{AB}
CoSe 03234	124.39 ^{BC}	101.85 ^{BCD}	1.78 ^{AB}	2.82	281.78 ^{AB}	22.53 ^A	270.00 ^{CD}	52.83 ^{AB}	125.01 ^{AB}	24.46 ^{AB}	10.04 ^{ABC}	44.19 ^{BC}
UP 05125	87.81 ^D	79.64 ^E	1.25 ^{CD}	2.54	229.33 ^{CD}	22.17 ^A	160.00 ^F	24.33 ^F	74.08 ^{CD}	11.23 ^F	7.23 ^D	39.27 ^C
CoS03251	109.57 ^{BCD}	104.79 ^{BCD}	1.18 ^{CD}	2.37	233.33 ^{CD}	19.93 ^C	186.67 ^E	50.63 ^{ABC}	86.43 ^{CD}	23.44 ^{ABC}	8.05 ^{CD}	45.97 ^{AB}
Co 098014	128.10 ^B	120.99 ^B	1.53 ^{BC}	2.41	304.11 ^A	21.87 ^A	298.33 ^{AB}	36.34 ^E	138.13 ^A	16.83 ^E	8.38 ^{BCD}	45.10 ^B
Co 0118	109.26 ^{BCD}	79.17 ^E	1.48 ^{BC}	2.61	245.55 ^{BCD}	22.33 ^A	208.33 ^E	46.93 ^{BCD}	96.46 ^{BC}	21.73 ^{BCD}	9.10 ^{ABCD}	45.02 ^B
CoLk 011201	116.21 ^{BC}	84.42 ^{DE}	0.96 ^D	2.37	210.11 ^D	20.70 ^{BC}	116.67 ^G	31.28 ^{EF}	54.02 ^D	14.48 ^{EF}	8.21 ^{BCD}	39.80 ^C
CoLk 013201	122.84 ^{BC}	110.50 ^{BC}	1.28 ^{CD}	2.53	253.11 ^{BCD}	20.07 ^C	251.67 ^D	37.17 ^{DE}	83.19 ^{CD}	17.54 ^{DE}	10.98 ^A	47.31 ^{AB}
CoPk 05191	160.50 ^A	145.22 ^A	1.48 ^{BC}	2.64	247.11 ^{BCD}	20.87 ^{BC}	306.67 ^A	59.57 ^A	141.99 ^A	27.61 ^A	10.02 ^{ABC}	50.10 ^A
Mean	117.87	101.91	1.47	2.60	252.10	21.35	230.56	42.26	103.04	19.60	9.14	44.83
CV(%)	11.79	11.57	19.49	10.65	10.24	2.69	6.11	14.29	20.84	13.98	13.54	6.41

Table 2: Means and analysis of variance for 12 yield and quality traits among 9 genotypes of sugarcane ratoon crop.

Correlation analysis

The analysis of variance affirmed significant difference for all the quality traits except brix% suggesting the presence of genetic variability among the different genotypes. Broad genetic distance indicates the hidden potential of the genotypes to be utilized for heterotic crossing F1 and transgressive segregants / genotypes. The improved high yielding varieties always have enormous space to facilitate production efforts for any commercial crop. At the same time, it is also significant to portray promising germplasm for selection of superior parents for creating wide spectrum of genetic variability in the population (Arrey and Mih, 2016).

Euclidean distance can be used to quantify the extent of genetic similarity or dissimilarity between parents so as transgressive genotypes can be exploited (Hoque and Rahman, 2006). Evaluation of genetic variability is helpful in crop improvement programme and hence, more efficient plant genotypes need to be isolated for the cultivation under different eco-environment. The genetic distance values of the 09 sugarcane genotypes are presented in Table 3. The greater genetic distance of 239.401 was found between CoPk 05191 and Co S 03251, followed by CoPk 05191 and UP 05125 (201.355), Co 098014 and CoS 03251 (178.029). CoLk 013201 and CoS 03251 (175.313), CoPk 05191 and Co 0238 (167.474), CoPk 05191 and CoLk 011201 (158.712) and Co 098014 and UP 05125 (145.768).

Variety	Co 0238	CoSe 03234	UP 05125	CoS03251	Co 098014	Co 0118	CoLk 011201	CoLk 013201	CoPk 05191
Co 0238	0.00
CoSe 03234	40.55	0.00
UP 05125	84.38	100.32	0.00
CoS03251	104.7	129.46	43.71	0.00
Co 098014	83.89	57.68	145.76	178.02	0.00
Co 0118	44.76	28.32	77.09	107.96	78.02	0.00	.	.	.
CoLk 011201	83.29	82.68	56.59	97.07	113.25	62.86	0.00	.	.
CoLk 013201	104.98	67.77	137.69	175.31	58.31	72.87	98.63	0.00	.
CoPk 05191	167.47	129.59	201.35	239.40	98.92	137.55	158.71	65.744	0.00

Table 3: Genetic distance between sugarcane genotypes based on metric and qualitative traits in first crop.

Furthermore, moderate genetic distance of 137.693 was found between CoLk 013201 and UP 05125, followed by CoPk 05191 and Co 0118 (137.552), CoPk 05191 and CoSe 03234 (129.595) and CoS 03251 and CoSe 03234 (129.465). Minimum distance was obtained between Co 0118 and CoSe 03234 (28.321), followed by CoSe 03234 and Co 0238 (40.555), Co S 03251 and UP 05125 (43.718), Co 0118 and Co 0 238 (44.762) and CoLk011201 and UP 0 5125 (56.599), respectively.

Grouping of genotypes in the cluster is one of the most important statistical analyses, which helps in clustering of genotypes based on genetic distance existing in various traits. Dendrogram was drawn from the cluster analysis of nine sugarcane genotypes based on twelve morpho-physiological characters as shown in Fig 1. Cluster analysis grouped the sugarcane genotypes into three clusters. Cluster one composed of four sugarcane genotypes such as, Co 0238, CoSe 03234, Co 0118 and CoLk 011201. Cluster two consisted of two sugarcane genotypes namely UP 05125 and CoS 03251; however, cluster three also contained three genotypes viz. Co 098014, CoLk 013201 and CoPk 05191. The relationship among the genotypes of a cluster had no correspondence with their geographical origin. This suggested that the genotypes of different geographical origin had genetic similarity being in one cluster and the genotypes of the same geographical origin had different genetic back ground, further suggesting that a high proportion of gene exchange might have occurred between the genotypes of diverse origin. Similar, results were also observed by Ram and Hemaprabha (1998) and Tahir *et al.* (2014) and they found the progenies of a cross clustered independently from their parents. Hence, this strategy can be employed to broaden the narrow genetic pool of sugarcane in India for further improvement of metric and quality traits. The same set of nine

sugarcane varieties were also evaluated in ratoon crop during 2016-17 for studying their genetic diversity and characters association.

The value of genetic distance of the nine sugarcane genotypes is presented in Table 4. The largest genetic distance of 227.923 was observed between CoPk 05191 and Co Lk 011201, followed by Co 098014 and CoLk 011201 (224.618), CoPk 05191 and UP 05125 (194.063), Co Lk 011201 and CoSe 03234(186.144) and CoLk 0 11201 and Co 0238 (185.611). Medium genetic distance of 179.927 was found between Co 098014 and UP 05125, followed by CoPk 05191 and CoS 03251 (148.407), CoLk 013201 and Co Lk 0 11201 (147.506), Co 098014 and CoS03251 (144.948) UP 05125 and CoSe 03234 (142.463), CoPk05191 and Co 0118 (137.683) and UP 05125 and Co 0238 (136.024). The least distance was recorded between the genotypes CoSe 03234 and Co0238 (33.840) followed by Co 0118 and CoS 03251 (37.425), Co 098014 and CoSe 03234 (46.777), CoS03251 and UP 05125 (53.639), CoLk 013201 andCoSe 03234 (57.399), CoLk 011201 and UP 05125 (59.510), CoLk013201 and Co 0238 (60.148) and Co 098014 and Co 0238 (61.454), respectively.

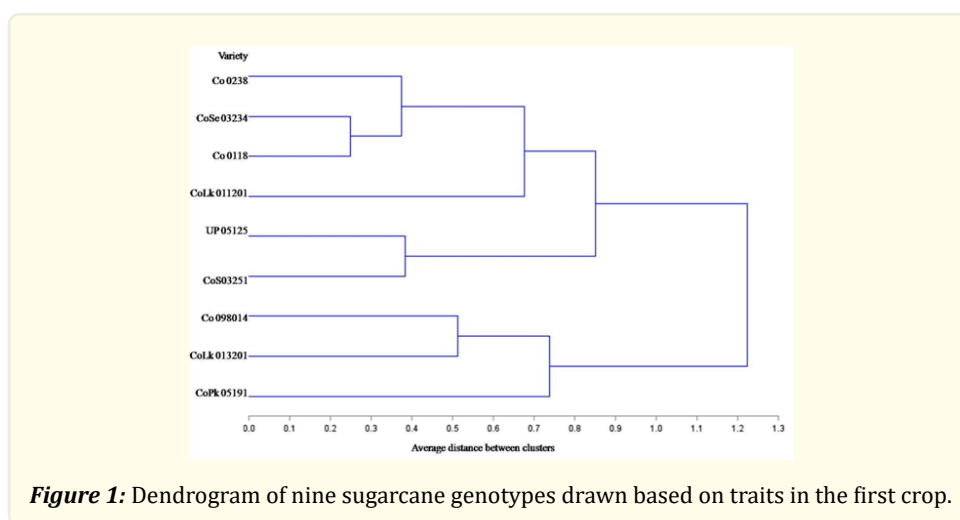
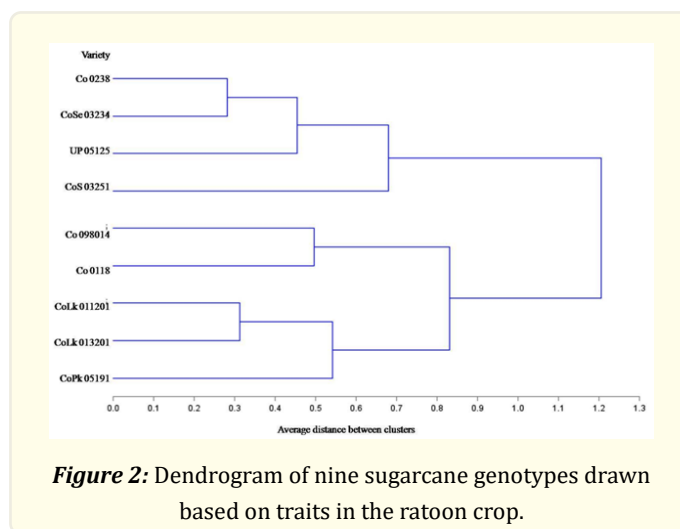


Figure 1: Dendrogram of nine sugarcane genotypes drawn based on traits in the first crop.

Variety	Co 0238	CoSe 03234	UP 05125	CoS 03251	Co 098014	Co 0118	CoLk 011201	CoLk 013201	CoPk 05191
Co 0238	0.00
CoSe 03234	33.84	0.00
UP 05125	136.02	142.46	0.00
CoS 03251	105.72	105.01	53.63	0.00
Co 098014	61.45	46.77	179.92	144.94	0.00
Co 0118	79.07	81.96	64.94	37.42	124.52	0.00	.	.	.
CoLk 011201	185.61	186.14	59.51	86.26	224.61	108.92	0.00	.	.
CoLk 013201	60.14	57.39	107.32	71.14	89.16	58.34	147.50	0.00	.
CoPk 05191	90.56	78.18	194.06	148.40	75.19	137.68	227.92	98.768	0.00

Table 4: Genetic distance between sugarcane genotypes based on metric and qualitative traits in ratoon crop.

The Dendrogram was obtained from cluster analysis of 09 sugarcane genotypes depicted in Fig 2. The cluster analysis categorized the genotypes into four clusters. Cluster one composed of three genotypes, viz; Co 0238, CoSe 03234 and Co098014. Cluster two also had three clones CoLk 013201, Co0118 and CoS 03251. Cluster three contained UP 05125 and CoLk 011201, whereas CoPk 05191 alone was in fourth cluster. Clustering pattern of the genotypes revealed that there is no correspondence between geographical and genetic diversity among the genotypes. The greater genetic distance between genotypes is the sole indicator of their greater genetic diversity lower distance reveals similar gene proximity among clones. The distantly related parents are expected to produce wide spectrum of genetic variability in segregating population which offers greater chances of selecting transgressive clones for evolving new cultivars. These findings covenant to those of Ram and Hemaprabha (1998), Tahir *et al.* (2014) and Baloch *et al.* (2017).



Correlation coefficients between quantitative characters and Brix were worked out to ascertain the relationship among the characters studied. The value of genotypic correlation coefficient in first plant crop is presented in Table 5, which reflected that cane yield (tonnes/ha) had highly significant positive correlation with cane height (0.948**), Single cane weight (0.817**), stem girth (0.753**), number of millable cane (0.695**), tillering (0.614**), green top yield (0.635**), LAI (0.510**) SPAD (0.738**) and Brix (0.418**). A similar association between cane yield, NMC, single cane weight, cane girth and cane height was also reported by Brown *et al.* (1969), Punia *et al.* (1983), Tyagi and Lal (2007) and Tena *et al.* (2016). It was also observed from the correlation analysis that cane yield was more closely linked with cane height, single cane weight, cane girth, number of millable cane and tillering count. The green top yield was found positively correlated with cane yield, tillering count, number of millable cane, single cane weight, sugarcane girth, cane height except Brix per cent.

The information from the Table 5 indicates that most characters affect cane yield but the magnitude of the characters which affect cane yield is dependent upon the degree of association of the characters with cane yield. In this case, selection for the characters such as number of millable cane and single cane weight would produce maximum cane and green top yield in comparison to any of the other characters. Choudhary and Joshi (2005), Kumar and Kumar (2014) and Brown *et al.* (1969) also highlighted the importance of selection for number of millable cane and single cane weight for higher cane yield, cane height, which had significant and positive association with cane girth, single cane weight, NMC and tillering count. Brix showed negative association with tillering count, number of millable cane, green top yield, LAI and SPAD. Similar relationship was also observed by Khan (1995). However, a negative association existed between Brix and green top yield, Brix and LAI, Brix and SPAD, Brix and tillering and Brix and NMC.

	1	2	3	4	5	6	7	8	9	10	11	12
1	1.000	0.9186**	-0.0095	-0.117	0.414	-0.275	0.639**	0.645**	0.615**	0.651**	0.634**	0.769**
2		1.000	0.0555	-0.165	0.546*	-0.387	0.748**	0.538*	0.695**	0.545*	0.464	0.842**
3			1.000	0.951**	0.663**	0.506*	0.724**	0.319	0.818**	0.316	0.489	0.408
4				1.000	0.419	0.434	0.647**	0.348	0.754**	0.342	0.923**	0.391
5					1.000	0.523*	0.945**	0.327	0.949**	0.330	0.289	0.397
6						1.000	0.177	-0.078	0.418	-0.092	-0.123	-0.305
7							1.000	0.569*	0.999**	0.573*	0.776**	0.897**
8								1.000	0.631**	0.999**	0.563*	0.818**
9									1.000	0.636**	0.511*	0.738**
10										1.000	0.583*	0.832**
11											1.000	0.817**
12												1.000

Where; 1=Tillering count; 2=number of millable cane (NMC); 3=Single cane weight; 4=sugarcane girth; 5=cane height; 6=brix%; 7=cane yield/plant; 8=green top yield/plot; 9=cane yield t/ha; 10=green top yield t/ha; 11=leaf area index; 12=SPAD reading

Table 5: Genotypic correlation coefficient among 12 different traits in nine sugarcane genotypes of first crop.

The characters' association of ratoon crop Table 6 revealed that one of the most crucial characters cane yield had a strong positive and highly significant correlation with all quantitative and physiological traits except Brix per cent. The correlation of cane yield was very strong with green top yield ($r= 0.993^{**}$), cane height ($r= 0.923^{**}$), number of millable cane/ NMC ($r = 0.748^{**}$) and tillering count ($r = 0.722^{**}$). In fact, a positive and highly significant correlation between cane yield and its components viz. NMC, cane height, single cane weight was also reported by Brown *et al.* (1969), Punia *et al.* (1983), Tyagi and Lal (2007) and Tena *et al.* (2016). This has important implications for selection of clones to be used as a parental material for crossing purposes. Hogarth (1971), James (1971) and Choudhary and Singh (1994) found that cane yield was more closely correlated with cane population than cane diameter. Brix % had a significant negative correlation with cane yield, green top yield, leaf area index, SPAD, tillering count, NMC and cane girth. Khan (1995) also observed negative association of NMC and Brix percent. Cane height showed positive and significant association with tillering count, NMC and single cane weight, while cane girth was significantly positive correlated with single cane weight and negatively correlated with NMC and tillering count Table 6.

	1	2	3	4	5	6	7	8	9	10	11	12
1	1.000	0.999**	-0.118	-0.252	0.463*	-0.735**	0.718**	0.628**	0.722**	0.628**	0.685**	0.289
2		1.000	-0.149	-0.368	0.466*	-0.680**	0.745**	0.722**	0.749**	0.722**	0.706**	0.422*
3			1.000	0.956**	0.673**	0.423*	0.527*	0.184	0.527*	0.183	0.611**	0.722**
4				1.000	0.381	-0.025	0.191	0.178	0.195	0.177	0.489	0.941**
5					1.000	0.278	0.926**	0.306	0.923**	0.306	0.869**	0.410
6						1.000	-0.127	-0.505	-0.138	-0.505**	-0.483	-0.449
7							1.000	0.643	0.844	0.643	0.883	0.734
8								1.000	0.653	0.999	0.685	0.634
9									1.000	0.653**	0.887**	0.740**
10										1.000	0.685**	0.633**
11											1.000	0.863**
12												1.000

Where; 1=Tillering count; 2=number of millable cane (NMC); 3=Single cane weight; 4=sugarcane girth; 5=cane height; 6=brix%; 7=cane yield/plant; 8=green top yield/plot; 9=cane yield t/ha; 10=green top yield t/ha; 11=leaf area index; 12=SPA

Table 6: Genotypic correlation coefficient among 12 different traits in nine sugarcane genotypes of ratoon crop.

Conclusion

The clustering pattern of the sugarcane genotypes revealed that the genetic relationships among the genotypes of a cluster have nothing to do with their geographical origin. The sugarcane genotype CoPk 05191 had considerable genetic distance from CoS03251, UP 05125, CoLk 011201, and Co 0118. Hence, these clones can further be exploited for hybridization programme in order to get transgressive and heterotic genotypes for higher cane as well as sugar yield. The association among the morpho-physiological characters implied that number of millable cane, green top yield and cane height, single cane weight, stem girth and brix were the most important characters for cane and sugar yield improvement. The four characters viz. number of millable cane (NMC), green top yield, single cane weight and cane height had highly significant positive correlation with cane and sugar yield. Thus, the above four characters need to be taken in to consideration while making selection for further improvement of cane and sugar yield.

References

1. Alwala S., et al. "Target region of amplification polymorphism (TRAP) for assessing genetic diversity in sugarcane germplasm Collections". *Crop Sci* 46 (2006): 448-55.
2. Arrey DB and Mih AM. "Characterization of five Sugarcane hand races in Western Cameroon". *American J. Bio. Life Science* 4 (2016): 33-40.
3. Baloch AW., et al. "Genetic Diversity Analysis in Commercial Sugarcane Genotypes". *Pak. J. Biotchnol* 14 (2017): 167-71.
4. Brown AHD, Daniels J and Latter BHD. "Quantitative Genetics of Sugarcane. Correlation Analysis of Continuous character in relation to Hybrid Sugarcane Breeding". *Theoretical Applied Genetics* 39 (1969): 01-10.
5. Choudhary AK and Singh JRP. "Correlation and path Coefficient Studies in Early Maturing clones of Sugarcane (*Saccharum spp. Complex*)". *Cooperative Sugar* 25 (1994): 305-07.
6. Choudhary RR and Joshi BK. "Correlation and path coefficient Analysis in Sugarcane". *Nepal Agricultural Research Journal* 6 (2005): 24-27.
7. Directorate of Economics and Statistics, Govt. of India, Ministry of Agriculture and Farmers Welfare (2019-20).
8. Henry RJ and Kole C. "Genetics, genomics and breeding of sugarcane". Enfield, New Hampshire: Science Publishers (2010).
9. Hogarth OM. "Quantitative Inheritance studies in Sugarcanes". *Australian Journal of Agricultural Research*, 22 (1971): 103-09.
10. Hoque M and Rahman L. "Estimation of Euclidian distance for different morpho-physiological characters in some wild and cultivated rice genotypes". *Pak Sci* 1 (2006): 77-09.
11. James NI. "Yield Components in Random and Selected Sugarcane Population". *Crop Science* 11 (1971): 906-08.
12. Khan KA. "Studies on Association among yield and quality character in Advanced Clones in Sugarcane". MSc Thesis, GB Pant University of Agriculture and Technology, Pantnagar (1995).
13. Khan IA., et al. "Environmental interactions of sugarcane genotypes and yield stability analysis of sugarcane". *Pak. J. Bot* 45.5 (2013): 1617-1622.
14. Kumar S and Kumar D. "Correlation and Path Coefficient Analysis in Sugarcane Germplasm under Subtropics". *African Journal of Agricultural Research* 9 (2014): 148-53.
15. Mahalanobis PC. "On the generalized distance in statistics". *Proc. Nat. Inst. Sci (Indian)* 2 (1936): 49-55.
16. Prakash D, Kamat DN and Krishna B. "Assessment of Genetic Diversity in Mid-late Maturing Sugarcane Clones under Waterlogging Condition in Lower Indo-gangetic Plains". *International Journal of Current Microbiology and Applied Science* 9.7 (2020): 1826-1833.
17. Punia MS, Paroda R and Hood RS. "Correlation and Path Analysis of Cane yield in Sugarcane". *Indian Journal of Genetics and Plant Breeding* 43 (1983): 109-12.
18. Ram B and Hemaprabha G. "Nature and pattern of genetic divergence of sugar yield and its components in the progenies of *Saccharum barberi*". *Indian J. Gen. Plant Breed* 58 (1998): 193-99.
19. Sanghera GS., et al. "Genetic Divergence among Elite Sugarcane Clones (*Saccharum officinarum L.*) based on cane yield and qual-

- ity traits from northern India". Journal of Experimental Biology and Agricultural Sciences 3.2 (2015): 185-190.
20. Sanghera GS., et al. "Genetic divergence among elite sugarcane clones (*Saccharum officinarum* L.) based on cane yield and quality traits from northern India". Indian Journal of Experimental Biology 1.3 (2015): 184-90.
 21. Sanghera GS., et al. "Quality parameters and their association with cane yield in sugarcane under subtropical conditions". Proceedings of National Symposium on Crop Improvement for Inclusive Sustainable Development held at Punjab Agricultural University, Ludhiana during (2014): 796-798.
 22. Santos JM., et al. "Genetic diversity of the main progenitors of sugarcane from the RIDESA germplasm Bank using SSR markers". Indian Crop Proc 40 (2012): 145-50.
 23. Singh P and Singh VP. "Genetic divergence in sugarcane germplasm". Indian Journal of Agricultural Sciences 72 (2002): 252-253.
 24. Tahir M., et al. "Character Association and Selection Indices in Sugarcane". American Journal of Experimental Agriculture 4 (2014): 336-48.
 25. Tena E, Mekbib F and Ayana A. "Correlation and path Coefficient Analysis in Sugarcane". Genotypes of Ethiopia 7 (2016): 1490-97.
 26. Tyagi AP and Lal P. "Correlation and Path Coefficient Analysis in Sugarcane". South Pacific Journal of Natural Science 25 (2007): 1-9.

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